

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/186,269ADATE: 09/08/94  
TIME: 17:28:05

INPUT SET: S3560.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ENTERED

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Bendig, Mary M.  
Leger, Olivier J.  
Saldanha, Jose  
Jones, S. Tarran

(ii) TITLE OF INVENTION: Humanized Antibodies Against Leukocyte  
Adhesion Molecule VLA-4

(iii) NUMBER OF SEQUENCES: 45

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Townsend and Townsend Kourie and Crew  
(B) STREET: One Market Plaza, Steuart Tower, Suite 2000  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94105

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/186,269  
(B) FILING DATE: 25-JAN-1994  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Smith, William L.  
(B) REGISTRATION NUMBER: 30,223  
(C) REFERENCE/DOCKET NUMBER: 15270-14

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-543-9600  
(B) TELEFAX: 415-543-5043

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

# RAW SEQUENCE LISTING PATENT APPLICATION US/08/186,269A

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47      (A) LENGTH: 483 base pairs
48      (B) TYPE: nucleic acid
49      (C) STRANDEDNESS: double
50      (D) TOPOLOGY: linear
51
52      (ii) MOLECULE TYPE: cDNA
53
54
55      (ix) FEATURE:
56          (A) NAME/KEY: CDS
57          (B) LOCATION: 53..430
58
59
60      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
61
62      ATGAGGGCCC CTGCTCAGAT TTTTGGATTC TTGGTCAGGA GACGTTGTAG AA ATG      55
63                                     Met
64                                     1
65
66      AGA CCG TCT ATT CAG TTC CTG GGG CTC TTG TTG TTC TGG CTT CAT GGT      103
67      Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His Gly
68          5                      10                      15
69
70      GCT CAG TGT GAC ATC CAG ATG ACA CAG TCT CCA TCC TCA CTG TCT GCA      151
71      Ala Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
72          20                      25                      30
73
74      TCT CTG GGA GGC AAA GTC ACC ATC ACT TGC AAG ACA AGC CAA GAC ATT      199
75      Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Thr Ser Gln Asp Ile
76          35                      40                      45
77
78      AAC AAG TAT ATG GCT TGG TAC CAA CAC AAG CCT GGA AAA CGT CCT AGG      247
79      Asn Lys Tyr Met Ala Trp Tyr Gln His Lys Pro Gly Lys Arg Pro Arg
80          50                      55                      60                      65
81
82      CTG CTC ATA CAT TAC ACA TCT GCA TTA CAG CCA GGC ATC CCA TCA AGG      295
83      Leu Leu Ile His Tyr Thr Ser Ala Leu Gln Pro Gly Ile Pro Ser Arg
84          70                      75                      80
85
86      TTC AGT GGA AGT GGG TCT GGG AGA GAT TAT TCC TTC AAC ATC AGC AAC      343
87      Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Asn Ile Ser Asn
88          85                      90                      95
89
90      CTG GAG CCT GAA GAT ATT GCA ACT TAT TAT TGT CTA CAG TAT GAT AAT      391
91      Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn
92          100                      105                      110
93
94      CTG TGG ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGGGCTGATG      440
95      Leu Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
96          115                      120                      125
97
98      CTGCACCAAC TGTATCCATC TTCCCACCAT CCACCCGGGA TCC      483
99

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RAW SEQUENCE LISTING  
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100 (2) INFORMATION FOR SEQ ID NO:2:

101

102 (i) SEQUENCE CHARACTERISTICS:

103 (A) LENGTH: 126 amino acids

104 (B) TYPE: amino acid

105 (D) TOPOLOGY: linear

106

107 (ii) MOLECULE TYPE: protein

108

109 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

110

111 Met Arg Pro Ser Ile Gln Phe Leu Gly Leu Leu Leu Phe Trp Leu His

112 1 5 10 15

113

114 Gly Ala Gln Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser

115 20 25 30

116

117 Ala Ser Leu Gly Gly Lys Val Thr Ile Thr Cys Lys Thr Ser Gln Asp

118 35 40 45

119

120 Ile Asn Lys Tyr Met Ala Trp Tyr Gln His Lys Pro Gly Lys Arg Pro

121 50 55 60

122

123 Arg Leu Leu Ile His Tyr Thr Ser Ala Leu Gln Pro Gly Ile Pro Ser

124 65 70 75 80

125

126 Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe Asn Ile Ser

127 85 90 95

128

129 Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp

130 100 105 110

131

132 Asn Leu Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

133 115 120 125

134

135

136 (2) INFORMATION FOR SEQ ID NO:3:

137

138 (i) SEQUENCE CHARACTERISTICS:

139 (A) LENGTH: 470 base pairs

140 (B) TYPE: nucleic acid

141 (C) STRANDEDNESS: double

142 (D) TOPOLOGY: linear

143

144 (ii) MOLECULE TYPE: cDNA

145

146

147 (ix) FEATURE:

148 (A) NAME/KEY: CDS

149 (B) LOCATION: 1..420

150

151

152 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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153
154 ATG AAA TGC AGC TGG GTC ATG TTC TTC CTG ATG GCA GTG GTT ACA GGG      48
155 Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly
156   1              5              10              15
157
158 GTC AAT TCA GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG      96
159 Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
160              20              25              30
161
162 CCA GGG GCC TCA GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT      144
163 Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
164              35              40              45
165
166 AAA GAC ACC TAT ATA CAC TGT GTG AAG CAG AGG CCT GAA CAG GGC CTG      192
167 Lys Asp Thr Tyr Ile His Cys Val Lys Gln Arg Pro Glu Gln Gly Leu
168   50              55              60
169
170 GAG TGG ATT GGA AGG ATT GAT CCT GCG AAT GGT TAT ACT AAA TAT GAC      240
171 Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Tyr Thr Lys Tyr Asp
172   65              70              75              80
173
174 CCG AAG TTC CAG GGC AAG GCC ACT ATA ACA GCT GAC ACA TCC TCC AAC      288
175 Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
176              85              90              95
177
178 ACA GCC TAC CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC      336
179 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
180              100              105              110
181
182 TAT TTC TGT GCT AGA GAG GGA TAT TAT GGT AAC TAC GGG GTC TAT GCT      384
183 Tyr Phe Cys Ala Arg Glu Gly Tyr Tyr Gly Asn Tyr Gly Val Tyr Ala
184              115              120              125
185
186 ATG GAC TAC TGG GGT CAA GGA ACC TCA GTC ACC GTC TCCTCAGCCA      430
187 Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
188   130              135              140
189
190 AAACGACACC CCCATCTGTC TATCCACTGG CCCGGGATCC      470
191
192
193 (2) INFORMATION FOR SEQ ID NO:4:
194
195     (i) SEQUENCE CHARACTERISTICS:
196         (A) LENGTH: 140 amino acids
197         (B) TYPE: amino acid
198         (D) TOPOLOGY: linear
199
200     (ii) MOLECULE TYPE: protein
201
202     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
203
204 Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly
205   1              5              10              15

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206
207 Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
208           20           25           30
209
210 Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
211           35           40           45
212
213 Lys Asp Thr Tyr Ile His Cys Val Lys Gln Arg Pro Glu Gln Gly Leu
214           50           55           60
215
216 Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Tyr Thr Lys Tyr Asp
217           65           70           75           80
218
219 Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
220           85           90           95
221
222 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
223           100          105          110
224
225 Tyr Phe Cys Ala Arg Glu Gly Tyr Tyr Gly Asn Tyr Gly Val Tyr Ala
226           115          120          125
227
228 Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
229           130          135          140
230
231 (2) INFORMATION FOR SEQ ID NO:5:
232
233 (i) SEQUENCE CHARACTERISTICS:
234 (A) LENGTH: 106 amino acids
235 (B) TYPE: amino acid
236 (C) STRANDEDNESS: single
237 (D) TOPOLOGY: linear
238
239 (ii) MOLECULE TYPE: protein
240
241
242
243 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
244
245 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
246 1           5           10           15
247
248 Gly Lys Val Thr Ile Thr Cys Lys Thr Ser Gln Asp Ile Asn Lys Tyr
249           20           25           30
250
251 Met Ala Trp Tyr Gln His Lys Pro Gly Lys Arg Pro Arg Leu Leu Ile
252           35           40           45
253
254 His Tyr Thr Ser Ala Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
255           50           55           60
256
257 Ser Gly Ser Gly Arg Asp Tyr Ser Phe Asn Ile Ser Asn Leu Glu Pro
258           65           70           75           80

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**SEQUENCE VERIFICATION REPORT**  
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